

10/540092



Figure 1

10/540092

Core	1	2	3	4	5	6	
Sequence	LKAGGA	SGTTG	GELCIGG	TGD	RIELGEIE	LGGHS	
SafB1	97	-LYAGVVAVPVYP-78	-YTSGSTADPKG-220	-GEIWRGPSVAQGY-23	-LRTGDL-23	-NYYPQDLEL-163	-LPDLGLDSLALVELKHRIE-
SafB2	1247	-LEAGGVAVPLDP-64	-YTSGSTGQPKG-172	-GELFIGGAGVARGY-24	-YRTGDL-23	-FRIEFEEIE-121	-FFDLGGNSLLATRLATRLA-
SafA1	559	-LKAGGAYVPLDP-64	-YTSGSSGRPKG-173	-GELFIGGSGVARGY-24	-YRTGDL-23	-YRIELAEIE-121	-FFELGGNSLLAGRLVEELD-
SafA2	1668	-LKAGGAYVPLDP-67	-YTSGSTGTPKA-179	-GELFVGGVGLARGY-24	-YRTGDL-23	-YRVELGEIE-122	-FFEVGGTSLLLARLASRL-
SacA	483	-MACGGSYVPLSD-63	-FTSGSTGEPKG-172	-GELIIHGHGVAQGY-20	-YRTGDR-23	-FRVELGPVQ-121	-FLDIGGHSLSLTLTGILR-
SacB	524	-WQVGGIYVPLSK-63	-YTSGSTGKPKG-173	-GELLICGPGVSQGY-22	-YLTGDR-23	-HRIELGEIE-123	-FFQLGGHSILVARMVERIE-
SacC	515	-RAGHAFLPIDPR-62	-YTSGSTGVPKG-178	-GEIMLAGQNLARGY-21	-YATGDL-23	-HRIELNEVA-122	-FFEQGGNSILLTRLAGTLS-
FUNCTION	unknown	ATP binding	ATP binding	ATPase motif	ATP binding	4' phosphopantetheine binding	

Figure 2

10/540092

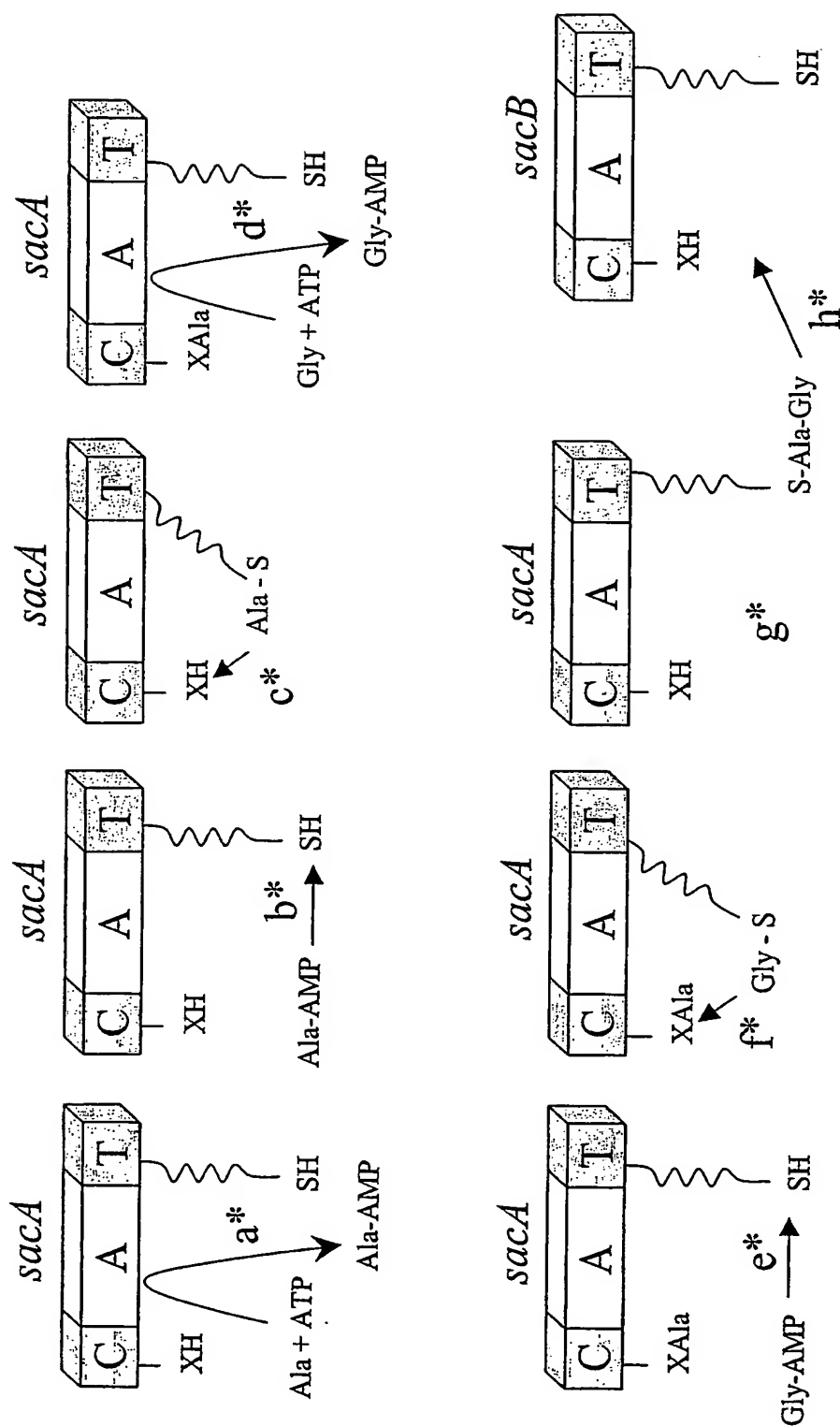


Figure 3

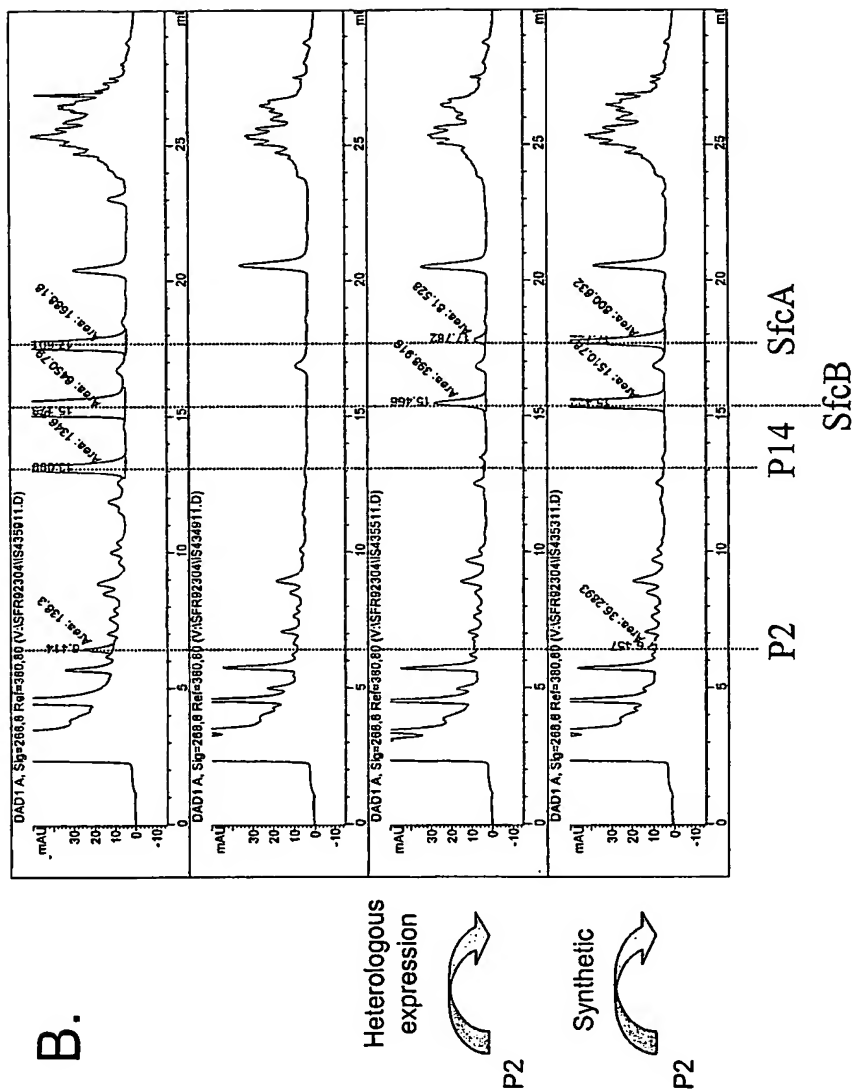
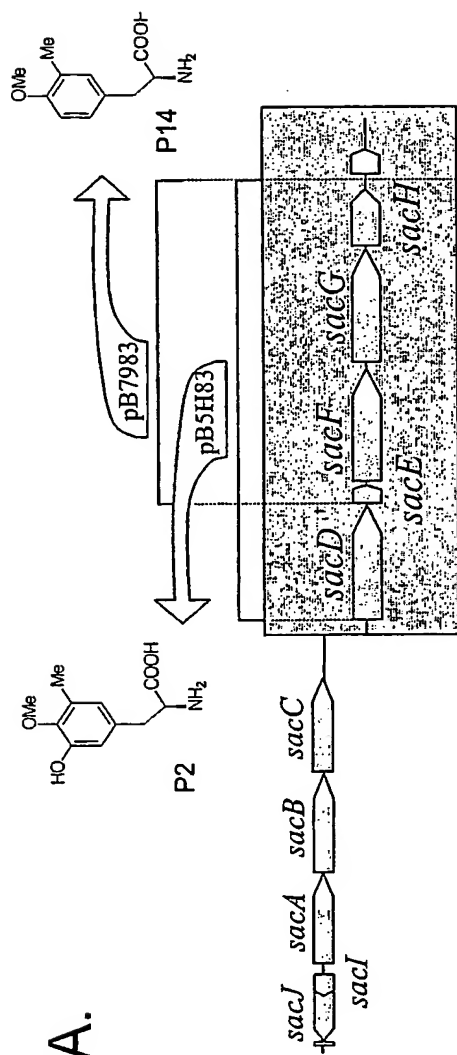


Figure 4

10 / 540092

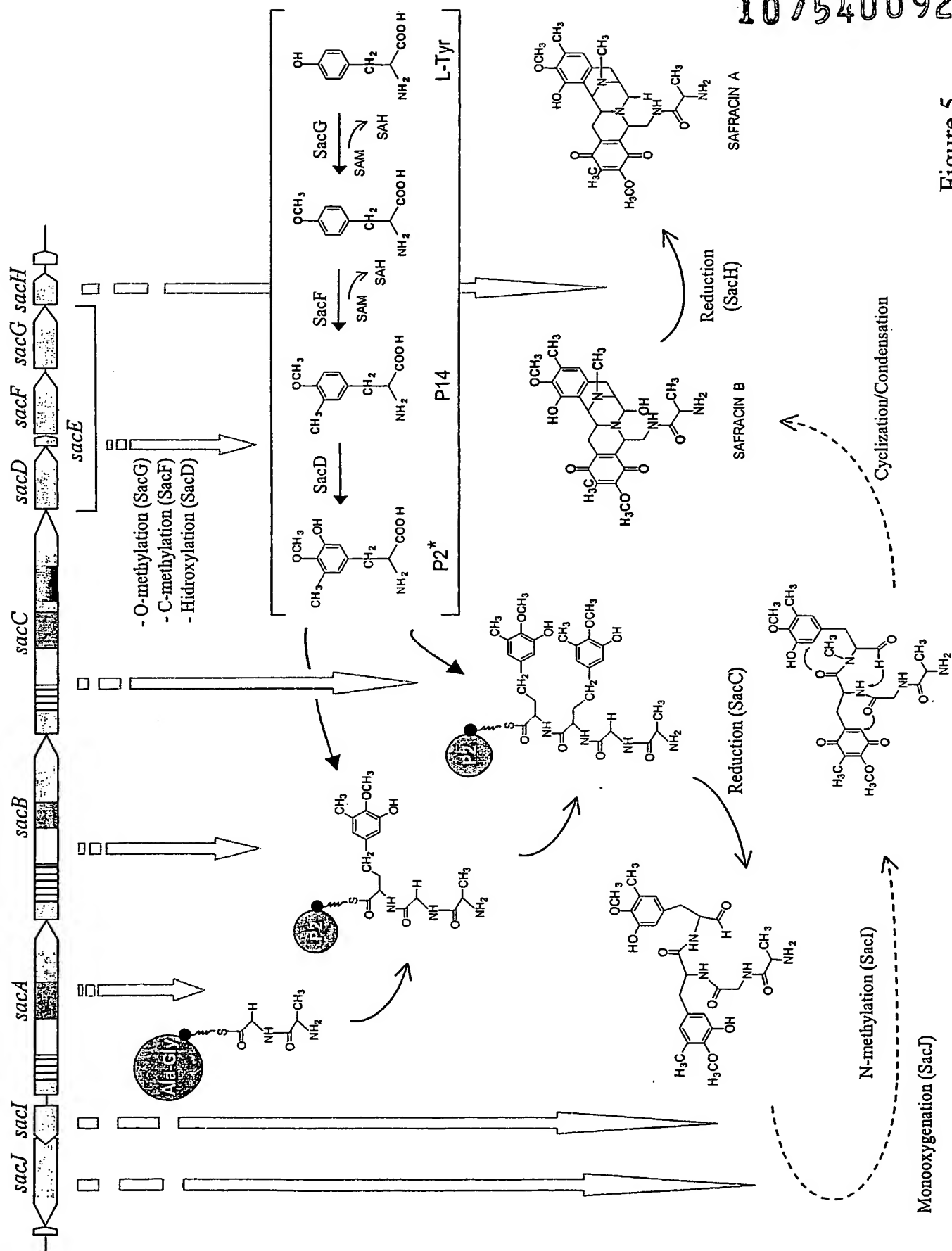


Figure 5

10/540092

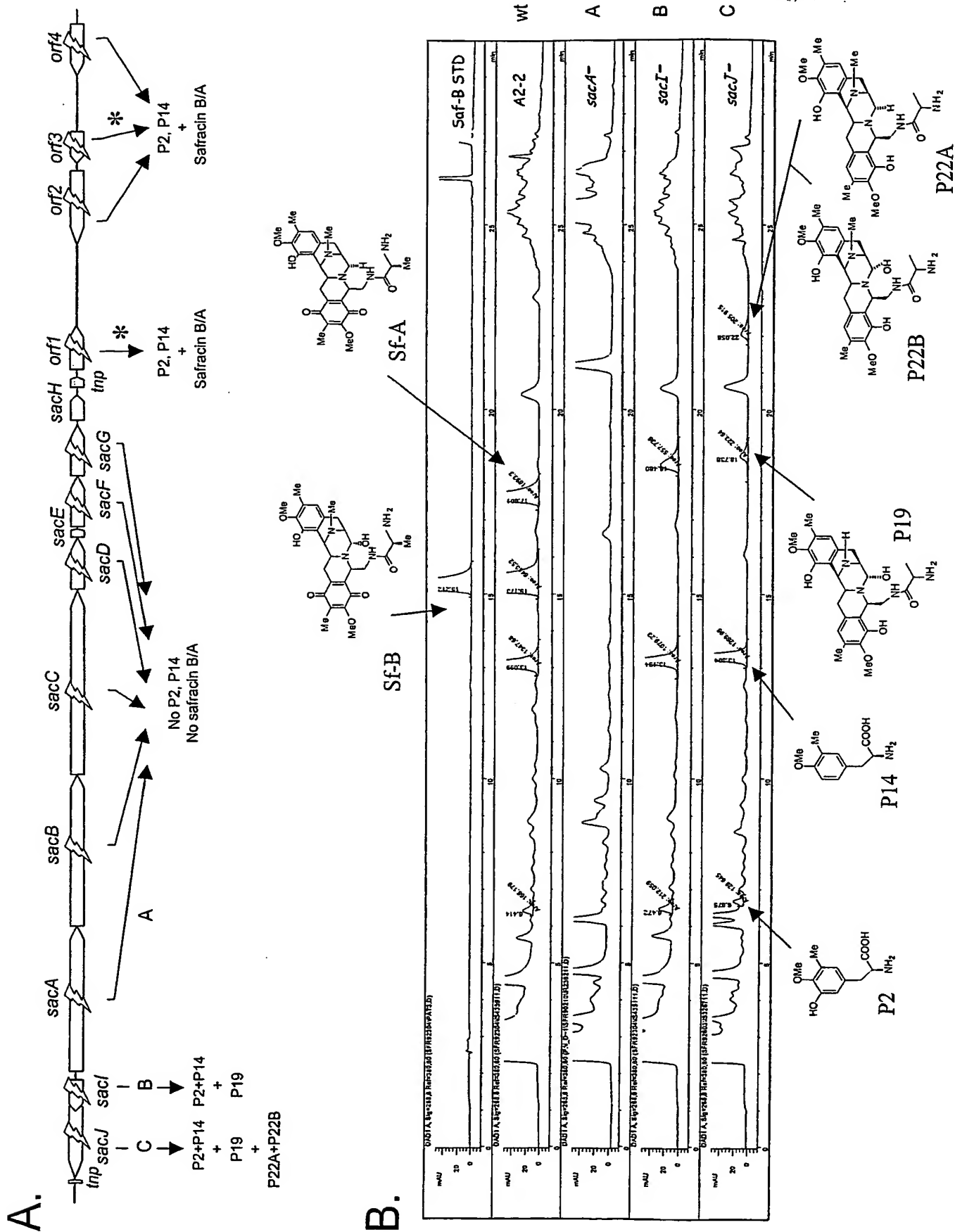


Figure 6

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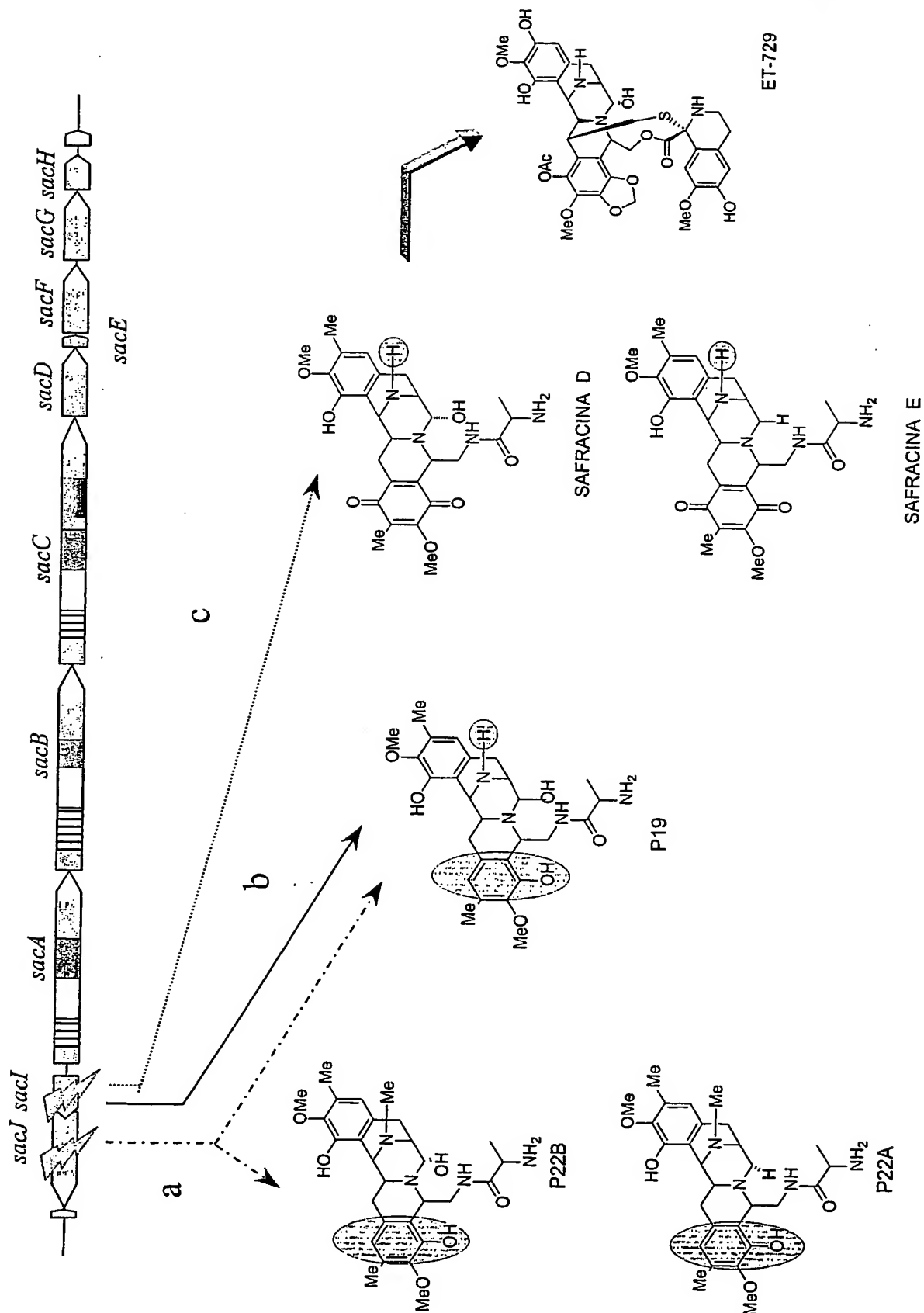


Figure 7

10/540092

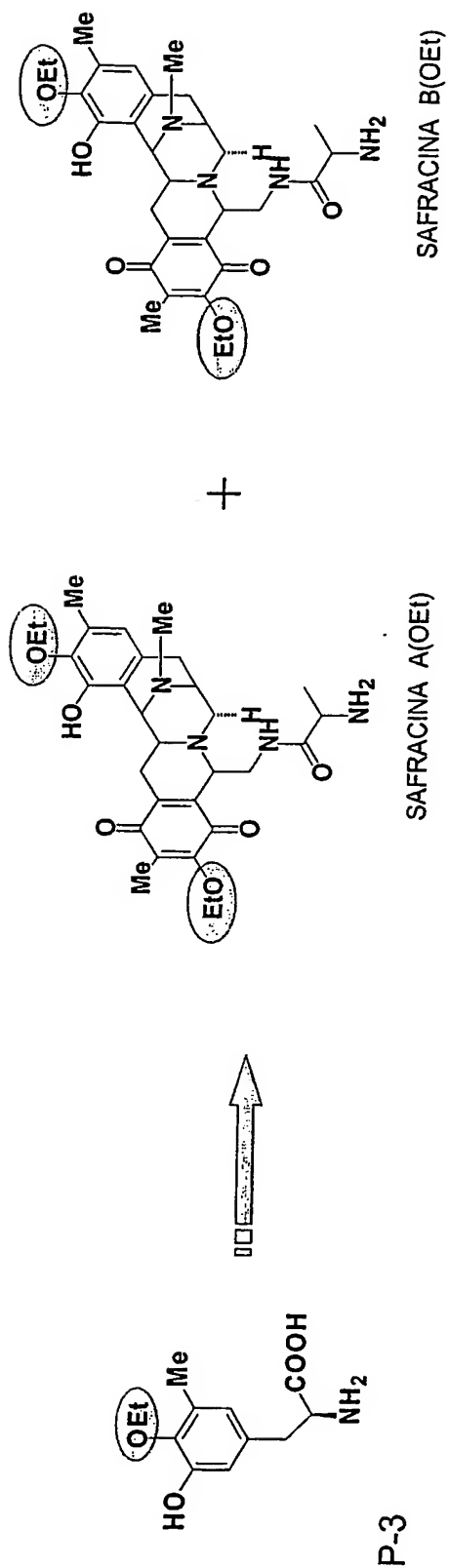


Figure 8

10/540092

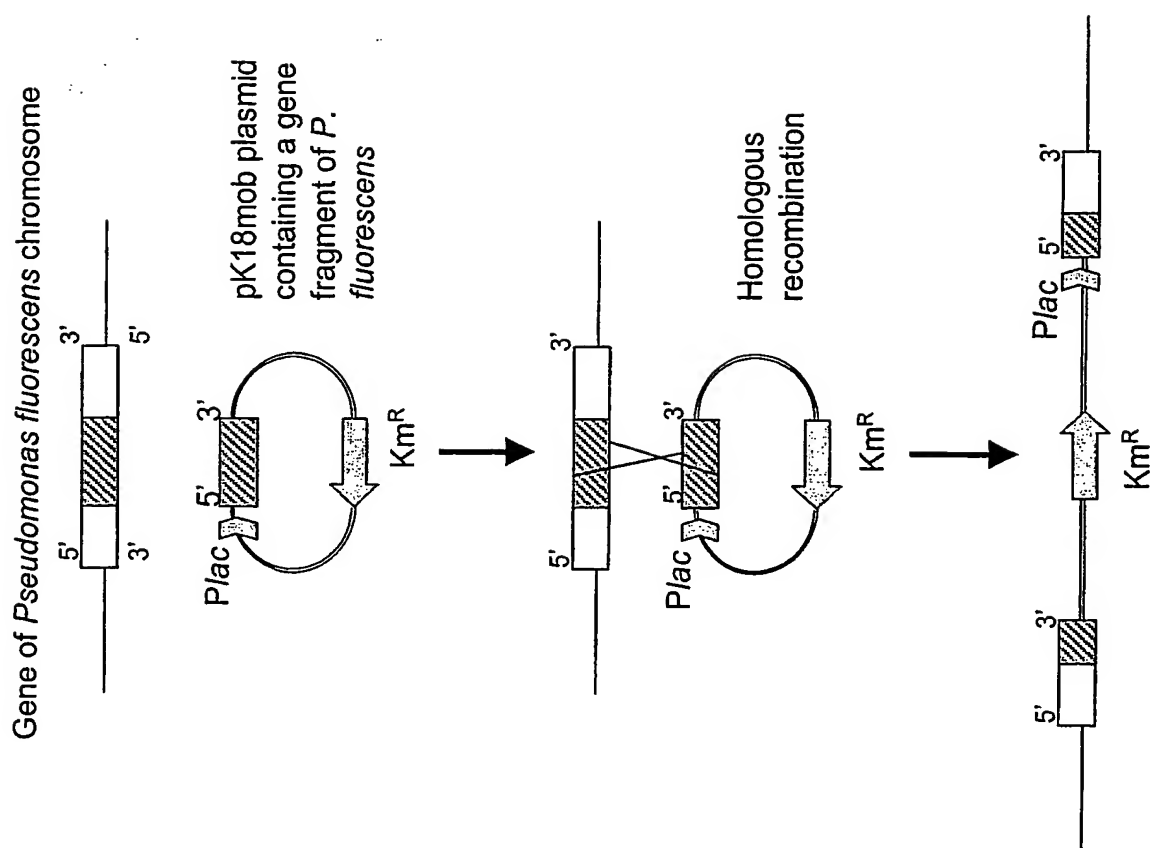


Figure 9